

Merging Revised Weights into Existing NHES Data Files

Data files for NHES:1999 that were downloaded or shipped prior to June 1st, 2001 contain weights that have subsequently been adjusted and need to be replaced. To create a system file containing the only revised weights, you will need to download the revised full ASCII data file and corresponding set-up file that extracts only the corrected weights and other variables necessary for merging into a SPSS, SAS or Stata system file. Old weights should be dropped from existing analysis files and the new weights merged in as replacements. Merging between your analysis files and the new weight file should be done using the variable BASMID as the match or key variable. The following examples demonstrate how to merge preexisting analysis files with the files containing the new weights using SAS, SPSS and Stata for the AE-NHES:1999, Parent-NHES:1999, and Youth-NHES:1999, respectively:

AE-NHES:1999

SAS code for merging analysis and weight files:

```
DATA ANALYSIS (DROP=FAWT FAWT1-FAWT80);  
SET analysis_filename;  
RUN;
```

```
PROC SORT DATA=ANALYSIS;  
BY BASMID;  
RUN;
```

```
PROC SORT DATA=weight_filename;  
BY BASMID;  
RUN;
```

```
DATA MERGED;  
MERGE ANALYSIS weight_filename;  
BY BASMID;  
RUN;
```

SPSS code for merging analysis and weight files:

```
GET FILE = 'analysis file' /DROP=FAWT TO FAWT80.  
SORT CASES BY BASMID.  
SAVE OUTFILE = 'TEMP'.
```

```
GET FILE = 'weight_filename'.  
SORT CASES BY BASMID.  
SAVE OUTFILE = 'TEMP2'.
```

```
MATCH FILES FILE = 'TEMP' /FILE = 'TEMP2'  
/BY BASMID.  
SAVE OUTFILE = 'MERGED'.
```

Stata code for merging analysis and weight files:

```
use "weights file", clear  
sort BASMID  
save "weights file", replace
```

```

use "analysis file", clear
drop FAWT FAWT1-FAWT80
sort BASMID
save "analysis file", replace

merge BASMID using "weights file"
ta _merge
drop _merge

```

Parent-NHES:1999

SAS code for merging analysis and weight files:

```

DATA ANALYSIS (DROP=FPWT FPWT1-FPWT80);
SET analysis_filename;
RUN;

```

```

PROC SORT DATA=ANALYSIS;
BY BASMID;
RUN;

```

```

PROC SORT DATA=weight_filename;
BY BASMID;
RUN;

```

```

DATA MERGED;
MERGE ANALYSIS weight_filename;
BY BASMID;
RUN;

```

SPSS code for merging analysis and weight files:

```

GET FILE = 'analysis file' /DROP=FPWT TO FPWT80.
SORT CASES BY BASMID.
SAVE OUTFILE = 'TEMP'.

```

```

GET FILE = 'weight_filename'.
SORT CASES BY BASMID.
SAVE OUTFILE = 'TEMP2'.

```

```

MATCH FILES FILE = 'TEMP' /FILE = 'TEMP2'
    /BY BASMID.
SAVE OUTFILE = 'MERGED'.

```

Stata code for merging analysis and weight files:

```

use "weights file", clear
sort BASMID
save "weights file", replace

```

```

use "analysis file", clear
drop FPWT FPWT1-FPWT80
sort BASMID
save "analysis file", replace

```

```

merge BASMID using "weights file"

```

```
ta _merge
drop _merge
```

Youth-NHES:1999

SAS code for merging analysis and weight files:

```
DATA ANALYSIS (DROP=FYWT FYWT1-FYWT80);
SET analysis_filename;
RUN;
```

```
PROC SORT DATA=ANALYSIS;
BY BASMID;
RUN;
```

```
PROC SORT DATA=weight_filename;
BY BASMID;
RUN;
```

```
DATA MERGED;
MERGE ANALYSIS weight_filename;
BY BASMID;
RUN;
```

SPSS code for merging analysis and weight files:

```
GET FILE = 'analysis file' /DROP=FYWT TO FYWT80.
SORT CASES BY BASMID.
SAVE OUTFILE = 'TEMP'.
```

```
GET FILE = 'weight_filename'.
SORT CASES BY BASMID.
SAVE OUTFILE = 'TEMP2'.
```

```
MATCH FILES FILE = 'TEMP' /FILE = 'TEMP2'
    /BY BASMID.
SAVE OUTFILE = 'MERGED'.
```

Stata code for merging analysis and weight files:

```
use "weights file", clear
sort BASMID
save "weights file", replace
```

```
use "analysis file", clear
drop FYWT FYWT1-FYWT80
sort BASMID
save "analysis file", replace
```

```
merge BASMID using "weights file"
ta _merge
drop _merge
```